

Resource Summary Report

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Trinity

RRID:SCR_013048

Type: Tool

Proper Citation

Trinity (RRID:SCR_013048)

Resource Information

URL: <http://trinityrnaseq.sourceforge.net/>

Proper Citation: Trinity (RRID:SCR_013048)

Description: Software for the efficient and robust de novo reconstruction of transcriptomes from RNA-seq data.

Abbreviations: Trinity

Resource Type: software resource

Defining Citation: [DOI:10.1038/nbt.1883](https://doi.org/10.1038/nbt.1883)

Keywords: bio.tools

Resource Name: Trinity

Resource ID: SCR_013048

Alternate IDs: biotools:trinity, OMICS_01327

Alternate URLs: <https://bio.tools/trinity>, <https://sources.debian.org/src/trinityrnaseq/>

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260821T193954+0000

Ratings and Alerts

No rating or validation information has been found for Trinity.

No alerts have been found for Trinity.

Data and Source Information

Usage and Citation Metrics

We found 10043 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Rock AQ, et al. (2026) Totipotency and high plasticity in an embryo with an invariant, fate-specifying cleavage program. *Current biology : CB*, 36(6), 1410.

Swift SZ, et al. (2026) Integration of Short- and Long-Read RNA Sequencing Enables the Discovery of Circular RNAs. *Cancer research*, 86(5), 1300.

Park J, et al. (2026) Innate immune priming by n-dodecyl- β -D-maltoside in murine models of bacterial and viral infection. *EBioMedicine*, 124, 106143.

Lv X, et al. (2026) *Blautia coccoides*-derived metabolite trimethylamine-N-oxide exacerbates Alzheimer's disease progression via targeting HIF1 α signaling. *Gut microbes*, 18(1), 2605768.

Mantzana-Oikonomaki V, et al. (2026) Pigments, Chromatophore Structure, and Gene Expression Underlying Colour Polytypy of a Panamanian Poison Frog. *Molecular ecology*, 35(1), e70214.

Hu L, et al. (2026) High-Resolution Genomic Resources for Trait Mapping and Precision Breeding for Adzuki Bean (*Vigna angularis*). *Advanced science (Weinheim, Baden-Wuerttemberg, Germany)*, 13(4), e07157.

Tan K, et al. (2026) Near-complete genome assembly of a transformation-efficient elite inbred line LH244 and its comparison with B73. *Journal of integrative plant biology*, 68(2), 366.

Witkowski RJ, et al. (2026) A Volatile Cue From a Specialist Herbivore Primes Gene Expression Against Biotic Stress in Tall Goldenrod (*Solidago altissima* L.). *Plant, cell & environment*, 49(3), 1424.

Zhang T, et al. (2026) Multi-omics analyses shed lights on the evolution and fruit development of Chinese raspberries (*Rubus* spp.). *Journal of integrative plant biology*, 68(4), 1032.

Zhang T, et al. (2026) ZmTH1 Is Vital for Healthy Plant Growth and Promotes Cold/Drought Tolerance by Regulating Thiamin Diphosphate-Dependent Metabolisms in Maize. *Plant biotechnology journal*, 24(3), 1234.

Xiang H, et al. (2026) Predominant mutated non-canonical tumor-specific antigens identified by proteogenomics demonstrate immunogenicity and tumor suppression in CRC. *Cell genomics*, 6(1), 101062.

Wu K, et al. (2026) Deciphering the role of ThHSF1 in the differential expression regulation of laccase isozymes in the white-rot fungus *Trametes hirsuta*. *Microbiology*

spectrum, 14(1), e0100425.

Wu L, et al. (2026) High-quality genome assembly and annotation of the white-cheeked goby, *Rhinogobius duospilus* (Herre, 1935) (Gobiiformes: Oxudercidae). *G3* (Bethesda, Md.), 16(2).

Sun D, et al. (2026) Chromosome-level genome assembly of the social amoeba *Heterostelium pallidum*. *Scientific data*, 13(1).

Mu Y, et al. (2026) Hormonal dynamics and transcriptomic regulatory mechanisms during seed dormancy release in *Aconitum kusnezoffii*. *PloS one*, 21(2), e0340761.

Pfeifer M, et al. (2026) High-quality haplotype-resolved genome assembly and annotation of *Malus baccata* 'Jackii'. *Scientific data*, 13(1), 14.

Allen GJP, et al. (2026) Neurometabolic rewiring in squid (*Sepioteuthis lessoniana*) optic lobes drives behavioral plasticity and visual integration under environmental acidification. *Communications biology*, 9(1), 229.

Hu QL, et al. (2026) Chromosome-level genome assembly of the predatory stink bug, *Eocanthecona furcellata* (Wolff). *Scientific data*, 13(1), 6.

Ma Y, et al. (2026) Transcriptomic differences in immune- and stress-related pathways associated with artificial rearing in the endangered hog deer (*Axis porcinus*). *BMC genomics*, 27(1), 196.

Li J, et al. (2026) A telomere-to-telomere genome assembly for *Cyperus difformis*. *Scientific data*, 13(1), 257.